

Amendments to the Specification:

-- The HPT1, hPEPT1, D2H, and hSI receptors were selected for cloning as GIT receptor targets based on several criteria, including: (1) expression on surface of epithelial cells in gastro-intestinal tract (GIT); (2) expression along the length of small intestine (HPT1, hPEPT1, D2H); (3) expression locally at high concentration (hSI); (4) large putative extracellular domains facing into the lumen of the GIT; and (5) extracellular domains that permit easy access and bioadhesion by targeting particles.

Receptor

D2H

hS1

HPT1

hPEPT1

The following receptor domains were cloned and expressed as His-tag fusion proteins by standard techniques:

Receptor

SEQ ID NOS

hPEPT1^a

391-571

16

HPT1^b

29-273

15

 hSi^c

272-667

14

- a Liang et al., 1995, J. Biol. Chem. 270: 6456-6463;
 b Dantzig et al., 1994, Association of Intestinal Peptide Transport with a Protein Related to the Cadherin Superfamily;
 c Chantret et al., Biochem. J. 285: 915-923;
 d Bertran et al., J. Biol. Chem. 268: 14842-14949.

The receptor proteins were expressed as His-tag fusion proteins and affinity purified under denaturing conditions, using urea or guanidine HCl, utilizing the pET His-tag metal chelate affinity for Ni-NTA Agarose (Hochuli, E., Purification of recombinant proteins with metal chelate adsorbent, Genetic Engineering, Principals and Methods (J.K. Setlow, ed.), Plenum Press, NY, Vol. 12 (1990), pp. 87-98).

As indicated in WO 98/51325, phage which showed specificity to a GIT receptor was further characterized by ELISA on a variety of recombinant proteins. Phage which continued to exhibit GIT receptor specificity was sequenced. Their insert sequences are summarized as follows:

| | | SEQ. |
|-----------------|--------------|---|
| <u>hSI</u> | <u>ID.NO</u> | <u>TARGET BINDING PHAGE INSERT SEQUENCE</u> |
| S15 | 17. | RSGAYESPDGRGGRSYVGGGGGCGNIGRKHNLWGLRTASPACWD |
| S21 | 18. | SPRSFWPVVSRHESFGISNYLGCGYRTCISGMTKSSPIYPRHS |
| S22 | 19. | SSSSDWGGVPGKVVRERFKGRGCGISITSVLTGKPNPCPEPKAA |
| Tui 40 Sni10 | 20. | RVGQCTDSDVRRPWARSCAHQCGAGTRNSHGCITRPLRQASAH |
| Sni28 | 21. | SHSGGMNRAYGDVFRELRDRWNATSHHTRPTPQLPRGPN |
| Sni34 | 22. | SPCGGSWGRFMQGGLFGGRTDGCGAHRNRTSASLEPPSSDY |
| Sni38 | 23. | RGAADQRRGWSENGLPRVGWDAIAHNSYTFTSRRPRPP |
| Sni45 | 24. | SGGEVSSWGRVNDLCARVSWTGCGTARSARTDNKGFLPKHSSLR |
| SniAX2 | 25. | SDSDGDHYGLRGGVRCSLRDRGCGGLALSTVHAGPPSFYPKLSSP |
| SniAX4 | 26. | RSLGNYGVTGTVDVTVLPMPGHANHLGVSSASSSDPPRR |

SniAX6 27. RTTTAKGCLLGSFGVLSGCSFTPTSPPPHLGYPHVS
SniAX8 28. SPKLSSVGVMKVTLPTEGPNAISIPISATLGPRNPLR

D2H

DAB3 29. RWCGAELCNSVTKKFRPGWRDHANPSTHHRTPPPSQSSP
DAB7 30. RWCGADDPCGASRWRGGNSLFGCGLRCSAAQSTPSGRIHSTSTS
DAB10 31. SKSGEGGDSSRGETGWARVRSHAMTAGRFRWYNQLPSDR
DAB18 32. RSSANNCEWKSDWMRRACIARYANSSGPARAVDTKAAP
DAB24 33. SKWSWSSRWGSPQDKVEKTRAGCGGSPSSTNCHPYTFAPPPQAG
DAB30 34. SGFWEFSRGLWDGENRKSVRSGCGFRGSSAQGPCVTPATIDKH
DAX15 35. SESGRCRSVSRWMTTWQTQKGGCGSNVSRGSPLDPSHQTGHATT
DAX23 36. REWRFAGPPLDLWAGPSLPSFNASSHPRALRTYWSQRPR
DAX24 37. RMEDIKN SGWRDSCRWGD LRP GCGSRQWYPSNMRSSRDYPAGGH
DAX27 38. SHPWYRHWNHGDFSGSGQSRHTPPESPHPGRPNATI
DCX8 39. RYKHDIGCDAGVDKKSSSVRGGCGAHSSPPRAGRGRGTMTVSRL
DCX11 40. SQGSKQCMQYRTGRLTVGSEYGCGMNP ARHATPAYPARLLPRYR
DCX26 41. SGRTTSEISGLWGWGDDRS GYGWGNTLRPNYIPYRQATNRHRYT
DCX33 42. RWNWTVLPATGGHYWTRSTDYHAINNHRPSIPHQHPTPI
DCX36 43. SWSSWNWSSKTTRLGDRATREGCGPSQSDGCPYNGRLTTVKPRT
DCX39 44. SGSLNAWQPRSWVGGAFRSHANNLNPKPTMVTRHPT
DCX42 45. RYSGLSPRDNGPACSQEATLEGCGAQRLMSTRRKGRNSRPGWTL
DCX45 46. SVGNDKTSRPVSFYGRVSDLWNASLMPKRT PSSKRHDDG

hPEPT1

PAX9 47. RWPSVG YKNGS DTIDVHSNDASTKRSLIYNHRRPLFP

PAX14 48. RTFENDGLGVGRSIQKKSDRWYASHNIRSHFASMSPAGK
 PAX15 49. SYCRVKGGGEGGHTDSNLARSGCGKVARTSRLQHINPRATPPSR
 PAX16 50. SWTRWKGKHTHGGFVNKSPPGKNATSPYTDAQLPSDQGPP
 PAX17 51. SQVDSFRNSFRWYEPSRALCHGCGKRDSTTRIHNPSDSYPTR
 PAX18 52. SFLRFQSPRFEDYSRTISRLRNATNPSNVSDAHNNRALA
 PAX35 53. RSITDGGINEVDLSSVSNVLENANSHRAYRKHRPTLKRP
 PAX38 54. SSKVSSPRDPTVPRKGGNVDYGCGHRSSARMPTSALSSITKCYT
 PAX40 55. RASTQGGRGVAPEFGASVLGRGCGSATYYTNSTSCKDAMGHNYS
 PAX43 56. RWCEKHKFTAARCSAGAGFERDASRPPQPAHRDNTNRNA
 PAX45 57. SFQVYPDHGLERHALDGTGPLYAMPGRWIRARPQNRDRQ
 PAX46 58. SRCTDNEQCPDTGTRSRSVSNARYFSSRLLKTHAPHRP
 P31 59. SARDSGPAEDGSRAVRLNGVENANTRKSSRSNPRGRRHP
 P90 60. SSADAIEKCAGSLLWWGRQNNSGCGSPTKKHLKHRNRSQTSSSSH
 5PAX3 61. RPKNVADAYSSQDGAAAEETSHASNAARKSPKHKPLRRP
 5PAX5 62. RGSTGTAGGERSGVLNLHTRDNASGSGFKPWYPSNRGHK
 5PAX7 63. RWGWERSPSDYDSDMDLGARRYATRTHRAPPVRLKAPLP
 5PAX12 64. RGWKCEGSQAAYGDKDIGRSRGCGSITKNNTNHAHPHSHGAVAKI

HPT-1

HAX9 65. SREEANWDGYKREMSHRSRFWDATHLSRPRRPANSGDPN
 HAX35 66. EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKPRK
 HAX40 67. REFAERRLWGCDDLSWRLDAEGCGPTPSNRAVKHRKPRPRSPAL
 HAX42 68. SDHALGTNLRSDNAKEPGDYNCCGNGNSTGRKVFNRRRPSAIP
 HCA3 69. RHISEYSFANSHLMGGESKRKGCGINGSFSPTCPRSPTPAFRRT
 H40 70. SRESGMWGSWWRGHRLNSTGGNANMNASLPPDPPVSTP
 PAX2 71. STPPSREAYSRPYSVDSDSDTNAKHSSHNRRLRTRSRPN